

1381 agatttggag gatttggggg ctgtagcccc cccagtcagt ggagacttaa ccaaagagga 1441 catagatetg attgacatec tttggcgaca ggatattgat etgggggetg ggcgtgaggt 1501 ttttgactat agtcaccgcc agaaggagca ggatgtggag aaggagctgc gagatggagg 1561 cgagcaggac acctgggcag gcgagggcgc ggaagctctg gcacggaacc tgctagtgga 1621 tggagagact ggggagagct tccctgcaca gtttccagca gacatttcca gcataacaga 1681 agcagtgcct agtgagagtg agcccctgc tcttcaaaac aacctcttgt ctcctcttct 1741 gaccgggaca gagtcaccat ttgatttgga acagcagtgg caagatctca tgtccatcat 1801 ggaaatgcag gccatggaag tgaacacatc agcaagtgaa atcctgtaca gtgcccctcc 1861 tggagaccca ctgagcacca actacagcct tgcccccaac actcccatca atcagaatgt 1921 cageetgeat caggegteec tgggggggetg cageeaggae ttettaetet teageecega 1981 ggtggaaagc ctgcctgtgg ccagtagctc cacgctgctc ccgttggccc ccagcaattc 2041 taccagette aactecacet teggeteeae caacetgaca gggetettet ttecacecea 2101 gctcaatggc acagccaatg acacagcagg cccagagctg cctgaccctt tgggggggtct 2161 gttagatgaa gctatgttgg atgagatcag ccttatggac ctggccattg aagaaggctt 2221 taaccetgtg caggeeteec agetggagga ggaatttgac tetgacteag geettteett 2281 agactegage catagecett etteectaag cagetetgaa ggeagttett eetettette 2341 etectectet teetettett eetetgette tteetetgee tetteeteet titetgagga 2401 aggtgeggtt ggetacaget etgactetga gaccetggat etggaagagg eegagggtge 2461 tgtgggctac cagcctgagt attccaagtt ctgccgcatg agctaccagg atccagctca 2521 geteteatge etgecetace tggageaegt gggecaeaae cacacataca acatggeaee 2581 cagtgeeetg gacteageeg acetgeeace acceagtgee etcaagaaag geageaagga 2641 gaagcagget gactteetgg acaagcagat gagcegggat gagcaccgag eccgagccat 2701 gaagateet tteaceaatg acaaaateat caacetgeet gtggaggagt teaatgaact 2761 gctgtccaaa taccagttga gtgaagccca gctgagcctc atccgagaca tccggcgccg 2821 gggcaagaac aagatggcgg cgcagaactg ccgcaagcgc aagctggaca ccatcctgaa 2881 tetggagegt gatgtggagg acetgeageg tgacaaagee eggetgetge gggagaaagt 2941 ggagtteetg egeteeetge gacagatgaa geagaaggte cagageetgt accaggaggt 3001 gtttgggcgg ctgcgagatg agaacggacg accetactcg cccagtcagt atgcgctcca 3061 gtacgccggg gacggcagtg tcctcctcat cccccgcacg atggccgacc agcaggcccg 3121 gcggcaggag aggaagccaa aggaccggag aaagtgagcc tggggaagaa gggggtttga 3181 ageccaccaa gaccgaaact ggagaaggge tggacctgga cetggacctg gacctacage 3241 ggggacttaa atgccttctt atccaatata tcttctcaga tgggatgact gcgggtcagt 3301 gtacaggaag aggcaggcac tggctggctc agctccactc gggtggagtg gaagtggcca 3361 gaccatttag acggacaggg tecteacect acceetttee tgtgaggeag gggtggtggt 3421 ggagttgctg gaggtagagg agctatgtgg agcaaaggcc gacagagggg aaggaatgga 3481 cctqtqaqaq gaagggaagg tggcagaaag tctcatttca ggaaggaggg atagaaggaa 3541 ggaaggaagg aaccccccc ccccgaaaa aaaaatcaaa gcgggaagaa aatcagaggg 3601 aaggttaagg ttggctctgg ccaggattcc aggcagcagg ttggagtgac tggtgggcct 3661 agatcactgg tgtgataaac cccatttcac cccggggggg gtggggtaca cagacacagg 3721 gtgggggtgg ggaggggcgg tgttaactct ttctgctcct tgcattttga catccctgaa 3781 ggggagetet tggatateat tggecatgtt teaategaat ggagecaetg ggececaaca 3841 ctggctttga gatttagagt caaagggtag agtgaacagg aaagggtcac gtggtcccat 3901 gttgcaacag ccccaacata cgcatgtcat tcactgcctt gccactccat ctccctccgt 3961 getecageca eccetgaget gaggetecca tigitetecat cagagecige atgigitatge 4021 cgtcctcccc tggtccggtg tttgtgttcc ccacccctca cagactgcct gagctcttct 4081 gtaagetggg gtagggtgat ggeagtgete egggaaetgg geetgeagee tteetettet 4141 gggactgctg tgaggcagag gaatgatgga gaatctagtg tagcagcctc caggcaggat 4201 teageacaac aetggggagt caecetteec tegggeetet geetaceaac aactgggett 4261 atcactggga aaacacaaaa aattacacaa cccagcaaca acaaaagaac tagtcctctt 4321 agaatttett gegetttgat tittttaggg ettgigeeet gitteaetta tagggietag 4381 aatgettgtg ttgagtaaaa aggagatgee caatatteaa agetgetaaa tgttetettt 4441 gecataaaga eteegtgtaa etgtgtgaae aettgggatt ttteteetet gteeegaggt 4501 cgtcgtctgc tttctttttt gggtttcttt ctagaagatt gagaagtgca tatgacaggc 4561 tgagageacc tececaaaca cacaagetet cagecacagg cagettetee acagececag 4621 cttcqcacaq gctcctggag ggctgcctgg gggaggcaga catgggagtg ccaaggtggc 4681 cagatggttc caggactaca atgtctttat ttttaactgt ttgccactgc tgccctcacc 4741 cctgcccggc tctggagtac cgtctgcccc agacaagtgg gagtgaaatg ggggtggggg 4801 gaagcactga ttcccaqtta gggggtgcct aactgagcag tagggataga aggtgtgaac 4861 ctgggagtgc ttttataaat tattttcctt gtagatttta tttttaattt atctctgtga NCBI Sequence Viewer

//

4981 aatggatgat to

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Oct 29 2003 07:23:28

(bits) Value Sequences producing significant alignments: gi|542952|pir||A49672 transcription factor Nrf1 - human >gi... 1210 0.0 gi|21748606|dbi|BAC03440.1| FLJ00380 protein [Homo sapiens] 0.0 <u>1200</u> gi|4505379|ref|NP 003195.1| nuclear factor (erythroid-deriv... <u>1195</u> 0.0 gi[31982173]ref[NP 032712.2] nuclear factor, erythroid deri... 0.0 <u>1166</u> gi|6831586|sp|061985|NFL1 MOUSE Nuclear factor erythroid 2 ... 1161 0.0

•		
gi[34873489]ref[XP 340887.1] similar to nuclear factor, ery	1143	0.0
gi[3978250]gb[AAC83235.1] Nrf1 splice variant D [Mus musculus]	1038	0.0
3	649	0.0
3-1	640	0.0
	<u>498</u>	e-139
	310	5e-83
gi 5441517 emb CAB46813.1 bZIP protein [Canis familiaris]		2e-79
gi 37682103 gb AA097978.1 nuclear factor-like 1 [Danio rerio]	<u>299</u>	
gi 3108203 gb AAC40108.1 nuclear factor erythroid-related	<u>295</u>	1e-78
gi 21918831 ref NP 004280.3 nuclear factor (erythroid-deri	<u>237</u>	7e-61
gi 20912933 ref XP 126805.1 similar to Nuclear factor eryt	<u>231</u>	3e-59
gi 33525212 gb AAH56142.1 NFE2L3 protein [Homo sapiens]	<u>231</u> -	4e-59
gi 4521225 dbi BAA76288.1 NF-E2-related factor 3 [Homo sap	228	4e-58 📖
gil29351561 gb AAH49219.11 NFE2L3 protein [Homo sapiens]	<u>226</u>	1e-57 L
gil6563268 gb AAF17228.1 NFE2-related factor 1 [Homo sapiens]	- <u>223</u>	1e-56 🗔
gi 37545874 ref XP 017121.4 similar to nuclear factor (ery	214	6e-54 🗔
gi 6754834 ref NP 035033.1 nuclear factor, erythroid deriv	198	3e-49
<u></u>	186	2e-45
9-10-10-00-00-1-0-1-0	182	2e-44
<u>911233113313333333</u>	182	2e-44
	182	2e-44
gi 33504557 ref NP 878309.1 nuclear factor (erythroid-deri		3e-44
gil6754832 ref NP 035032.11 nuclear, factor, erythroid deri	<u>182</u>	9e-44
gi 13929118 ref NP 113977.1 NF-E2-related factor 2 [Rattus	180	7e-43
gil2134328 pir 150224 erythroid cell transcription factor	<u>177</u>	_
gil27695228 gb AAH43997.1 Similar to nuclear factor (eryth	<u>176</u>	1e-42
gi 2136301 pir 159340 transcription factor Nrf2 - human >g	<u>175</u>	3e-42
gi 33469085 ref NP 032711.1 nuclear factor, erythroid deri	<u>174</u>	4e-42
gi 20903673 ref XP 128255.1 nuclear factor, erythroid deri	<u>174</u>	5e-42
gi 20149576 ref NP 006155.2 nuclear factor (erythroid-deri	<u>174</u>	5e-42
gil5453774 ref NP 006154.1 nuclear factor (erythroid-deriv	<u> 174</u> -	6e-42 l
gi 1082640 pir A54692 transcription factor NF-E2 45K chain	<u>172</u>	1e-41
gi 506818 gb AAA35612.1 leucine zipper protein	<u>172</u>	3e-41
gi 31200287 ref XP 309091.1 ENSANGP00000003712 [Anopheles	<u> 167</u>	7e-40
gi 28077099 ref NP 778208.1 nuclear factor (erythroid-deri	<u> 162</u>	2e-38 L
gi 24649238 ref NP 732834.1 cap-n-collar CG17894-PB [Droso	<u>153</u>	1e-35
gi 24649240 ref NP 732835.1 cap-n-collar CG17894-PA [Droso	<u>151</u>	4e-35
gi 24649236 ref NP 732833.1 cap-n-collar CG17894-PC [Droso	<u>151</u>	4e-35
gi 3859885 gb AAC72896.1 cap 'n' collar isoform A [Drosoph	151	4e-35
gi 7511827 pir T13936 collar protein isoform C - fruit fly	151	4e-35
gi 3859887 gb AAC72897.1 cap 'n' collar isoform B [Drosoph	<u>151</u>	5e-35
	150	1e-34
gi 103368 pir A33111 segmentation protein cnc - fruit fly	149	1e-34
gi 1352098 sp P20482 CNC DROME Segmentation protein cap'n'c gi 157074 gb AAB59246.1 segmentation protein [Drosophila m	148	3e-34
	129	3e-28
gi 34868687 ref XP 345884.1 similar to transcription facto	94	1e-17
gi 34867531 ref XP 221712.2 similar to Bach1 [Rattus norve		2e-17
gi 2565400 gb AAB84100.1 transcription regulator protein [<u>93</u>	
gil4502353 ref NP 001177.1 BTB and CNC homology 1, basic 1	<u>93</u>	2e-17
gi 6680764 ref NP 031546.1 BTB and CNC homology 1 [Mus mus	<u>92</u>	2e-17
gi 7768712 dbj BAA95505.1 transcription regulator protein	<u>92</u>	3e-17
<u>gi 13540490 ref NP 068585.1 </u> BTB and CNC homology 1, basic	<u>84</u>	9e-15
gi 13898847 gb AAK48898.1 BACH2 transcription factor [Homo	<u>84</u>	9e-15
gi 30109320 qb AAH51242.1 Similar to BTB and CNC homology	<u>84</u>	1e-14
gi 6671608 ref NP 031547.1 BTB and CNC homology 2 [Mus mus	<u>84</u>	1e-14
qi 2565402 qb AAB84101.1 Bach1 protein homolog [Homo sapiens]	<u>75</u>	5e-12
gi 34867221 ref XP 232858.2 similar to BTB and CNC homolog	<u>73</u>	2e-11
gi 5739132 gb AAD50356.1 Cap'n'collar protein [Thermobia d	<u>64</u>	1e-08 _
gi 25148068 ref NP 741404.1 the Binding Domain Of Skn-1 In	_57	1e-06 🔙
gi 25148072 ref NP 741406.1 the Binding Domain Of Skn-1 In	<u> 57</u>	1e-06 🗌
gi 25148077 ref NP 741405.1 the Binding Domain Of Skn-1 In	<u>57</u>	2e-06
GITESTROOT LOSTIN THEORY		

gil3318844 pdb 1SKN P Chain P, The Binding Domain Of Skn-1	<u>56</u>	3e-06 💆
gi 17565016 ref NP 503719.1 predicted CDS, the Binding Dom	_52	3e-05
gil15636685 gb AAL02138.1 transcription factor AP-1 [Branc	44	0.011
gil2497469 splP79703 JUNB CYPCA TRANSCRIPTION FACTOR JUN-B	44	0.014
gi 29823878 emb CAD56858.1 JunB protein [Takifugu rubripes]	43	0.023
	42	0.030
<u> </u>	42	0.031
<u> </u>	42	0.032
	42	0.032
gi 52759 emb CAA31252.1 unnamed protein product [Mus muscu		0.032
gil6680512 ref NP 032442.1 Jun-B oncogene [Mus musculus] >	42	
gi 31419519 gb AAH53234.1 Unknown (protein for MGC:64066)	42	0.032
gi 5650726 emb CAB51637.1 c-Jun protein [Xenopus laevis]	42	0.034
gi 31339308 dbj BAC77044.1 c-Jun protein [Carassius auratus]	<u>42</u>	0.034
gi]11177866 ref NP 068608.1 jun B proto-oncogene [Rattus n	<u>42</u>	0.035
gi 710348 gb AAA74916.1 transcription factor junB	<u>42</u>	0.035
gi 4504809 ref NP 002220.1 jun B proto-oncogene [Homo sapi	<u>42</u>	0.036
gi 14495707 gb AAH09465.1 Jun B proto-oncogene [Homo sapiens]	<u>42</u>	0.036
gi 29823874 emb CAD56856.1 c-Jun protein [Takifugu rubripes]	42	0.036
gi 3023298 sp P56432 AP1 PIG Transcription factor AP-1 (Act	42	0.037
gi 225973 prf 1404381A c-jun oncogene	42	0.037
gi 4758616 ref NP 002219.1 v-jun avian sarcoma virus 17 on	42	0.037
	42	0.037
<u>gi 226129 prf 1411298A</u> c-jun gene gi 6754402 ref NP 034721.1 Jun oncogene; activator protein	42	0.037
	42	0.037
gi 11177864 ref NP 068607.1 v-jun sarcoma virus 17 oncogen	42	0.037
gil68985 pir TVHUJN transcription factor AP-1 - human		0.037
gil135295 sp P18870 AP1 CHICK TRANSCRIPTION FACTOR AP-1 (PR	_42	
gi 21313434 ref NP 084356.1 RIKEN cDNA 1700012K17; androge	42	0.040
gi 12838749 dbj BAB24315.1 unnamed protein product [Mus mu	<u>42</u>	0.040

Alignments

transcription factor Nrf1 - human \Box >qi|542952|pir||A49672 gi|14714932|qb|AAH10623.1| NFE2L1 protein [Homo sapiens] Length = 742Score = 1210 bits (3131), Expect = 0.0Identities = 652/740 (88%), Positives = 652/740 (88%) MLSLKKYLTEGLLOFTILLSLIGVRVDVDTYLTSOLPPLREIILGPSSAYTOTOFHNLRN 60 Query: 1 MLSLKKYLTEGLLOFTILLSLIGVRVDVDTYLTSOLPPLREIILGPSSAYTOTOFHNLRN MLSLKKYLTEGLLOFTILLSLIGVRVDVDTYLTSQLPPLREIILGPSSAYTQTQFHNLRN 60 Sbict: 1 TLDGYGIHPKSIDLDNYFTARRLLSOVRALDRFOVPTTEVNAWLVHRDPEGSVSGSOPNS 120 Query: 61 TLDGYG1HPKS1DLDNYFTARRLLSQVRALDRFQVPTTEVNAWLVHRDPEGSVSGSQPNS Sbjct: 61 TLDGYGIHPKSIDLDNYFTARRLLSOVRALDRFOVPTTEVNAWLVHRDPEGSVSGSQPNS 120 Ouery: 121 GLALESSSGLODVTGPDNGVRESETEOGFGEDLEDLGAVAPPVSGDLTKEDIDLIDILWR 180 GLALESSSGLODVTGPDNGVRESETEOGFGEDLEDLGAVAPPVSGDLTKEDIDLIDILWR Sbjct: 121 GLALESSSGLODVTGPDNGVRESETEOGFGEDLEDLGAVAPPVSGDLTKEDIDLIDILWR 180

Ouery: 181 ODIDLGAGREVFDYSHROKEODVEKELRDGGEODTWAGEGAEALARNLLVDGETGESFPA 240

Sbjct: 181 ODIDLGAGREVFDYSHROKEODVEKELRDGGEODTWAGEGAEALARNLLVDGETGESFPA 240

ODIDLGAGREVFDYSHROKEODVEKELRDGGEODTWAGEGAEALARNLLVDGETGESFPA

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